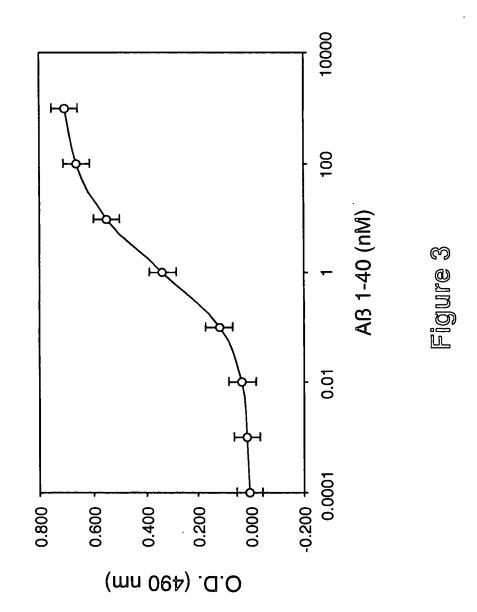
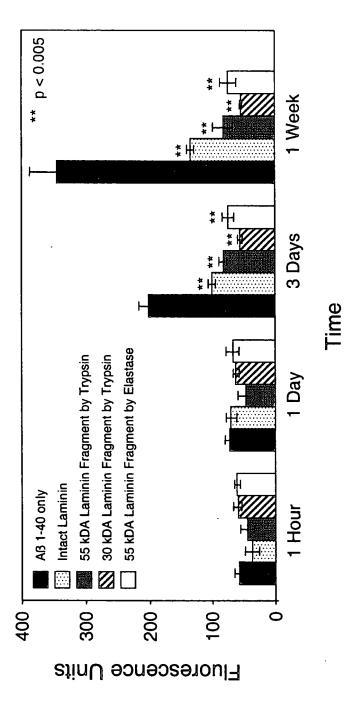


Figure 2





4 7

Figure 4

Figure 5

e 5

îs

152 TSISLYMKPPPKPOTTGAWVADOPVLYLGSKNAKKEYMGLAIKNDNLYYVYNLGMKDVEILLDSKPVSSWPAYFSIV A4G-1 A4G-2 A4G-3 A4G-4 A4G-5 A4G-6 A4G-7 A4G-8 A4G-9 A4G-10 XIERVGKHGKVFLTVPSSSSTAEEKFIKKGEFAGDDSLLDLTPEDTVFYVGGVPANFKLPASLNLPSYSGCLELATL

A4G-11 A4G-12 A4G-13 A4G-14 A4G-15 A4G-16 A4G-17 A4G-18 A4G-19 1006 NNDVISLYNFKHIYNMDPSKSVPCARDKLAFTQSRAASYFFDGSSYAVVRDITRRGKFGQVTRFDIEIRTPADNGLV A4G-20 A4G-21 A4G-22 A4G-23 A4G-24 A4G-25 A4G-26 A4G-27 A4G-28 LLMVNGSMFFSLEMRNGYLHVFYDFGFSNGPVHLEDTLKKAQINDAKYREISIIYHNDKKMILVVDRRHVKSTDNEK 1160 KKIPFTDIYIGGAPQEVLQSRTLRAHLPLDINFRGCMKGIQFQKKDPMLLBQTBTLGVGYGCPEDSLISRRAYFNGQ A4G-38 A4G-39 A4G-40 A4G-41 A4G-42 A4G-43 A4G-44 A4G-45 A4G-46 A4G-47 SFIASIQKISFFDGFEGGFNFRTLQPNGLLFYYTSGSDVFSISLDNGTVVNDVKGIKVMSTDKQYHDGLPHFVVTSI

A4G-48 A4G-49 A4G-50 A4G-51 A4G-52 A4G-53 A4G-54 A4G-55 A4G-56 1314 SDTRYELVVDKSRLRGKNPTKGKAEQTQTTEKKPYFGGSPISPQYANFTGCISNAYFTRLDRDVEVEAFQRYSEKVH A4G-57 A4G-58 A4G-59 A4G-60 A4G-61 A4G-62 A4G-63 A4G-64 A4G-65 A4G-66 TSLYECPIESSPLFLLHKKGKNSSKPKTNKQGEKSKDAPSWDPIGLKFLEQKAPRDSHCHLFSSPRAIEHAYQYGGT

A4G-67 A4G-68 A4G-69 A4G-70 A4G-71 A4G-72 A4G-73 A4G-74 A4G-75 ANSRQEFEHEQGDFGEKSQFSIRLKTRSSHGMIFYVSDQEENDFMTLFLAHGRLVFMFNVGHKKLKIRSQEKYNDGL 1515
WHDVIFIREKSSGRLVIDGLRVLEERLPPSGAAWKIKGPIYLGGVAPGRAVKNVQITSVYSFSGCLGNLQLNGASIT
A4G-86 A4G-87 A4G-88 A4G-89 A4G-90 A4G-91 A4G-92 A4G-93 A4G-94 SASQTFSVTPCFEGPMETGTYFSTEGGYVVLDESFNIGLKFEIAFEVRPRSSSGTLVHGHSVNGEYLNVHHRNGQVI

A4G-95 A4G-96 A4G-97 A4G-98 A4G-99 A4G-100 A4G-101 A4G-102 A4G-103 1699 VKVNNGVRDFSTSVTPKQNLCDGRWHRITVIRDSNVVQLDVDSEVNHVVGPLNPKPVDHREPVFVGGVPESLLTPRL A4G-104 A4G-105 A4G-106 A4G-107 A4G-108 A4G-109 A4G-110 A4G-111 A4G-112 1776 APSKPPTGCIRHFVIDSRPVSFSKAALVSGAVSINSCPTA A4G-113 A4G-114 A4G-115 A4G-116

44 P4

2679
TALKPHIQSPVPAPEPGKNTGDHFVLYMGSRQATGDYMGVSLRNQKVHWVYRLGKAGPTTLSIDENIGEQFAAVSIDR A5G-1 A5G-2 A5G-3 A5G-4 A5G-5 A5G-6 A5G-7 A5G-8 A5G-9 A5G-10 2758 TLQFGHMSVTVEKQMVHEIKGDTVAPGSEGLLNLHPDDFVFYVGGYPSNPTPPEPLRFPGYLGCIEMETLNEEVVSLY A5G-11 A5G-12 A5G-13 A5G-14 A5G-15 A5G-16 A5G-17 2835
NFEQTFMLDTAVDKPCARSKATGDPWLTDGSYLDGSGFARISFEKQFSNTKRFDQELRLVSYNGIIFFLKQESQFLCL
A5G-19 A5G-20 A5G-21 A5G-22 A5G-23 A5G-24 AG5-25 A5G-26 AG5-27 A5G-28 2913 AVQEGTLVLFYDFGSGLKKADPLQPPQALTAASKAIQVFLLAGNRKRVLVRVERATVFSVDQDNMLEMADAYYLGGVP A5G-29 A5G-30 A5G-31 A5G-32 A5G-33 A5G-34 A5G-35 A5G-36 A5G-37 A5G-38 שלטנ PEQLPLSLRQLFPSGGSVRGCIKGIKALGKYVDLKRLNTTGISFGCTADLLVGRTMTFHGHGFLPLALPDVAPITEVV A5G-39 A5G-40 A5G-41 A5G-42 A5G-43 A5G-44 A5G-45 A5G-46 A5G-47 3059 YSGPGFRGTQDNNLLYYRTSPDGPYQVSLREGHVTLRFMNQEVETQRVFADGAPHYVAFYSNVTGVWLYVDDQLQLVK A5G-48 A5G-49 A5G-50 A5G-51 A5G-52 A5G-53 A5G-54 A5G-55 3147 SHERTTPHLQLQPEEPSRLLLGGLPVSGTFHNFSGCISNVFVQRLRGPQRVFDLHQNHGSVNVSVGCTPAQLIETSRA A5G-57 A5G-58 A5G-59 A5G-60 A5G-61 A5G-62 A5G-63 A5G-64 A5G-65 A5G-66 ${\tt 32025} \\ {\tt TAQKVSRRSRQPSQDLACTTPWLPGTIQDAYQFGGPLPSYLQFVGISPSHRNRLHLSMLVRPHAASQGLLLSTAPMSG} \\ {\tt CARROLL STAPMSG} \\ {\tt CARROLL$ A5G-67 A5G-68 A5G-69 A5G-70 A5G-71 A5G-72 A5G-73 A5G-74 3303 RSPSLVLFLNHGHFVAQTEGPGPRLQVQSRQHSRAGQWBRVSVRWGMQQIQLVVDGSQTWSQKALHHRVPRAERPQPY A5G-76 A5G-77 A5G-78 A5G-79 A5G-80 A5G-81 A5G-82 A5G-83 A5G-84 A5G-85 3458 TLSVGGLPASSYSSKLPVSVGFSGCLKKLQLDKQPLRTPTQMVGVTPCVSGPLEDGLFFPGSEGVVTLELPKAKMPYV A5G-90 A5G-91 A5G-92 A5G-86 A5G-87 A5G-88 A5G-89 3459 SLELBHRPLAAAGLIFHLGQALATPYMQLKVLTEQVLLQANDGAGEFSTWVTYPKLCDGRWHRVAVIMGRDTLRLEVD A5G-94 A5G-95 A5G-96 A5G-97 A5G-98 A5G-99 A5G-100 3537 TQSNHTTGRLPESLAGSPALLHLGSLPKSSTARPELPAYRGCLRKLLINGAPVNVTASVQIQGAVGHRGCPSGTLALS A5G-103 A5G-104 A5G-105 A5G-106 A5G-107 A5G-108 A5G-109 A5G-110 A5G-111 3615 KQGKALTQRHAKPSVSPLLH A5G-112 A5G-113

44 64

Figure 7

PEPTIDES	Laminin Chain and Amino Acid Sequence Number	Amino Acid Sequence	% Disruption/ Disassembly of Fibrillar AB (AB:Peptide Molar Ratio of 1:6)
AG73	Alpha-1 chain; residues 2719-2730	RKRLQVQLSIRT	46 % (S; p < 0.01)***
A3	Alpha-3 chain; residues 2243-2254	KPRLQFSLDIQT	23 % (S; p < 0.01)
A5	Alpha-5 chain; residues 3275-3286	RNRLHLSMLVRP	22 % (S; p<0.01)
C-16	Gamma-1 chain; residues 139-150	KAFDITYVRLKF	28 % (S; p<0.01)***
LAM-L	Alpha-1 chain; residues 2097-2108	AASIKVAVSADR	24 % (S; p<0.01)
A-13	Alpha-1 chain; residues 97-109	RQVFQVAYIIIKA	30 % (S; p<0.01)***
HA3G45	Alpha-3 chain; residues 1173-1184	ASFGFQTFQPSG	21 % (S; p<0.05)
HA3G47	Alpha-3 chain; residues 1189-2000	HQTWTRNLQVTL	28 % (S; p<0.01)***
HA3G58	Alpha-3 chain; residues 1276-1287	ISNVFVQRLSLS	32 % (S; p<0.01)***
HA3G67	Alpha-3 chain; residues 1342-1353	ASPPSVKVWQDA	25 % (S; p<0.01)***
HA3G71	Alpha-3 chain; residues 1379-1390	FKLPQELLKPRS	23 % (S; p<0.05)
HA3G74	Alpha-3 chain; residues 1402-1414	RGLVFHTGTKNSF	32 % (S; p<0.01)***
HA3G75	Alpha-3 chain; residues 1411-1422	KNSFMALYLSKG	24 % (S; p<0.01)
HA3G76	Alpha-3 chain; residues 1418-1429	YLSKGRLVFALG	26 % (S; p<0.01)***
HA3G79	Alpha-3 chain; residues 1444-1455	NDGKWHTVVFGH	27 % (S; p<0.01)***
HA3G83	Alpha-3 chain; residues 1477-1487	GNSTISIRAPVY	33 % (S; p<0.01)***
A4G31	Alpha-4 chain; residues 1101-1112	LHVFYDFGFSNG	23 % (S; p<0.01)
A4G82	Alpha-4 chain; residues 1513-1524	TLFLAHGRLVFM	30 % (S; p<0.01)***
A5G15	Alpha-5 chain; residues 2792-2803	HPDDFVFYVGGY	30 % (S; p<0.01)***
A5G35	Alpha-5 chain; residues 2950-2961	VLVRVERATVFS	20 % (S; p<0.05)
A5G46	Alpha-5 chain; residues 3043-3054	FLPLALPDVAPI	21 % (S; p<0.05)
A5G56	Alpha-5 chain; residues 3135-3146	WLYVDDQLQLVK	27 % (S; p<0.01)***
A5G71	Alpha-5 chain; residues 3259-3270	GPLPSYLQFVGI	22 % (S; p<0.05)
A5G80	Alpha-5 chain; residues 3329-3340	VQSRQHSRAGQW	25 % (S; p<0.01)***
A5G81	Alpha-5 chain; residues 3337-3348	AGQWHRVSVRWG	41 % (S; p<0.01)***
A5G82	Alpha-5 chain; residues 3345-3356	VRWGMQQIQLVV	29 % (S; p<0.01)***
A5G84	Alpha-5 chain; residues 3361-3372	TWSQKALHHRVP	27 % (S; p<0.01)***
A5G101	Alpha-5 chain; residues 3516-3527	DGRWHRVAVIMG	39 % (S; p<0.01)***
A5G109	Alpha-5 chain; residues 3587-3598	APVNVTASVQIQ	32 % (S; p<0.01)***
A5G110	Alpha-5 chain; residues 3594-3605	SVQIQGAVGMRG	23 % (S; p<0.05)

*** Selected for Further Testing

Figure 8

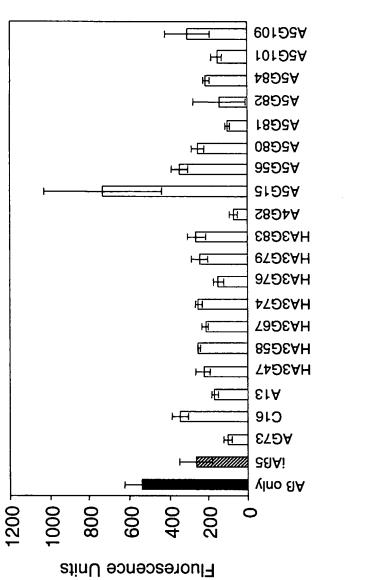
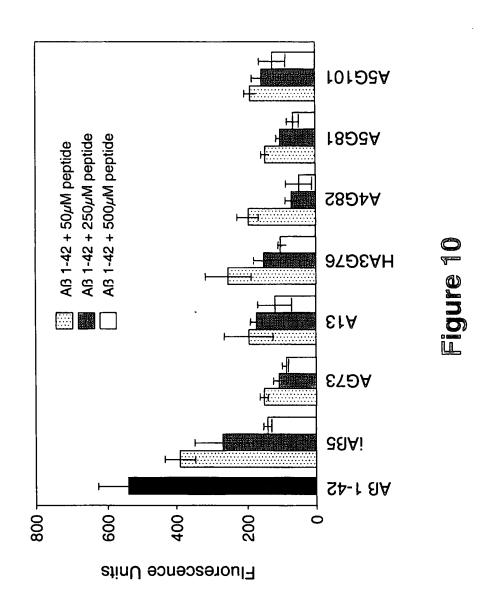


Figure 9



PTI-	•	Structure	Formula	MW
DP-001 D-AG73 or D-A1 A1-chain 2719-2730		Arg-Lys-Arg-Lue-Gln-Val-Gln-Leu-Ser-Ile-Arg-Thr	C ₆₄ H ₁₂₀ N ₂₄ O ₁₇	1497.82
DP-002 D-A13 A1-chain 97-109		Arg-Gln-Val-Phe-Gln-Val-Ala-Tyr-Ile-Ile-Ile-Lys-Ala	C74H121N19O17	1548.90
DP-003 D-HA3G76 A3-chain 1418-1429		Tyr-Leu-Ser-Lys-Gly-Arg-Leu-Val-Phe-Ala-Leu-Gly	C ₆₃ H ₁₀₂ N ₁₆ O ₁₅	1323.61
DP-004 D-A4G82 A4-chain 1513-1524		Thr-Leu-Phe-Leu-Ala-His-Gly-Arg-Leu-Val-Phe-Met	C ₆₇ H ₁₀₅ N ₁₇ O ₁₄ S	1404.75
DP-005 D-A5G81 A5-chain 3337-3348		Ala-Gly-Gln-Trp-His-Arg-Val-Ser-Val-Arg-Trp-Gly	C ₆₅ H ₉₅ N ₂₃ O ₁₅	1438.62
DP-006 D-A5G101 A5-chain 3516-3527		Asp-Gly-Arg-Trp-His-Arg-Val-Ala-Val-Ile-Met-Gly	C ₆₁ H ₉₇ N ₂₁ O ₁₅ S	1396.65
DP-007 D-HA3G47 A3-chain 1189-2000		His-Gln-Thr-Trp-Thr-Arg-Asn-Leu-Gln-Val-Thr-Leu	C ₆₆ H ₁₀₅ N ₂₁ O ₁₉	1496.70
DP-008 D-HA3G58 A3-chain 1276-1287		Ile-Ser-Asn-Val-Phe-Val-Gln-Arg-Leu-Ser-Leu-Ser	C ₆₁ H ₁₀₃ N ₁₇ O ₁₈	1362.60

Fig. 12a

PTI-	Structure	Formula	MW
DP-009 D-HA3G74 A3-chain 1402-1414	Arg-Gly-Leu-Val-Phe-His-Thr-Gly-Thr-Lys-Asn-Ser-Phe	C ₆₆ H ₁₀₂ N ₂₀ O ₁₈	1463.67
DP-010 D-HA3G83 A3-chain 1477-1487	Gly-Asn-Ser-Thr-Ile-Ser-Ile-Arg-Ala-Pro-Val-Tyr	C ₅₆ H ₉₂ N ₁₆ O ₁₈	1277.45
DP-011 D-A5G82 A5-chain 3345-3356	Val-Arg-Trp-Gly-Met-Gln-Ile-Gln-Leu-Val-Val	C ₆₆ H ₁₀₉ N ₁₉ O ₁₆ S	1456.78
DP-012 D-A5G109 A3-chain 1444-1455	Ala-Pro-Val-Asn-Val-Thr-Ala-Ser-Val-Gin-Ile-Gin	C ₅₃ H ₉₁ N ₁₅ O ₁₈	1226.40
DP-013 D-rAG73 or D-rA1 A1-chain r2719-2730 or 2730-2719	Thr-Arg-Ile-Ser-Leu-Gln-Val-Gln-Leu-Arg-Lys-Arg	C ₆₄ H ₁₂₀ N ₂₄ O ₁₇	1497.82
DP-014 D-rA13 A1-chain r92-109 or 109-92	Ala-Lys-Ile-Ile-Ile-Tyr-Ala-Val-Gln-Phe-Val-Gln-Arg	C74H121N19O17	1547.92
DP-015 D-rHA3G76 A3-chain r1418-1429 or 1429-1418	Gly-Leu-Ala-Phe-Val-Leu-Arg-Gly-Lys-Ser-Leu-Tyr	C ₆₃ H ₁₀₂ N ₁₆ O ₁₅	1323.61
DP-016 D-rA4G82 A4-chain r1513-1524 or 1524-1513	Met-Phe-Val-Leu-Arg-Gly-His-Ala-Leu-Phe-Leu-Thr	C ₆₇ H ₁₀₅ N ₁₇ O ₁₄ S	1404.75

Fig. 126

PTI-		Structure	Formula	MW
DP-017	,	Gly-Trp-Arg-Val-Ser-Val-Arg-His-Trp-Gln-Gly-Ala		
D-rA5G81 A5-chain r3337-3348 or 3348-3337		NINE ID AND AND AND AND AND AND AND AND AND AN	C ₆₅ H ₉₅ N ₂₃ O ₁₅	1438.62
DP-018	_	Gly-Met-Ile-Val-Ala-Val-Arg-His-Trp-Arg-Gly-Asp	· · · · · · · · · · · · · · · · · · ·	
D-rASG101 A5-chain r3516-3527 or 3527-3516	,	Oly-Mct-ne-vai-Ala-vai-Alg-nis-1rp-Arg-Gly-Asp	C ₆₁ H ₉₇ N ₂₁ O ₁₅ S	1396.65
LP-019 AG73 or AI AI-chain 2719-2730		Arg-Lys-Arg-Lue-Gln-Val-Gln-Leu-Ser-Ile-Arg-Thr	C ₆₄ H ₁₂₀ N ₂₄ O ₁₇	1497.82
LP-020 A13 A1-chain 92-109		Arg-Gln-Val-Phe-Gln-Val-Ala-Tyr-Ile-Ile-Ile-Lys-Ala	C ₇₄ H ₁₂₁ N ₁₉ O ₁₇	1548.90
LP-021 HA3G76 A3-chain 1418-1429		Tyr-Leu-Ser-Lys-Gly-Arg-Leu-Val-Phe-Ala-Leu-Gly	C ₆₃ H ₁₀₂ N ₁₆ O ₁₅	1323.61
LP-022 A4G82 A4-chain 1513-1524		Thr-Leu-Phe-Phe-Met-Arg-Leu-Val-His-Ala-Leu-Gly	C ₆₇ H ₁₀₅ N ₁₇ O ₁₄ S	1404.75
LP-023 A5G81 A5-chain 3337-3348		Ala-Gly-Gln-Trp-His-Arg-Val-Ser-Val-Arg-Trp-Gly	C ₆₅ H ₉₅ N ₂₃ O ₁₅	1438.62
LP-024 A5G101 A5-chain 3516-3527		Asp-Gly-Arg-Trp-His-Arg-Val-Ala-Val-Ile-Met-Gly Here are a second and the second are a second and the second are a second	C ₆₁ H ₉₇ N ₂₁ O ₁₅ S	1396.65

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Fig. 12c

PTI- LP-025 β-sheet breaker or iAβ5
DP-026 Trc'n 5;1-7
DP-027 Trc'n 5;2-8
DP-028 Trc'n 5;3-9
DP-029 Trc'n 5;4-10
DP-030 Trc'n 5;5-11
DP-031 Tre'n 5;6-12
DP-032 Trc'n 6;1-7

Structure	Formula	MW
Leu-Pro-Phe-Phe-Asp	C ₃₃ H ₄₃ N ₅ O ₈	637.74
Ala-Gly-Gln-Trp-His-Arg-Val	C ₃₈ H ₅₆ N ₁₄ O ₉	852.95
Gly-Gln-Trp-His-Arg-Val-Ser	C ₃₈ H ₅₆ N ₁₄ O ₁₀	868.95
Gln-Trp-His-Arg-Val-Ser-Val	C ₄₁ H ₆₂ N ₁₄ O ₁₀	911.04
Trp-His-Arg-Val-Ser-Val-Arg	C ₄₂ H ₆₆ N ₁₆ O ₉	939.09
His-Arg-Val-Ser-Val-Arg-Trp	C ₄₂ H ₆₆ N ₁₆ O ₉	939.09
Arg-Val-Ser-Val-Arg-Trp-Gly	C ₃₈ H ₆₂ N ₁₄ O ₉	859.00
Asp-Gly-Arg-Trp-His-Arg-Val	C ₄₀ H ₆₀ N ₁₆ O ₁₀	925.02

Fig. 12d

PTI-	Structure	Formula	MW
DP-033 Trc'n 6;2-8	Gly-Arg-Trp-His-Arg-Val-Ala	C ₃₉ H ₆₀ N ₁₆ O ₈	881.01
DP-034 Trc'n 6;3-9	Arg-Trp-His-Arg-Val-Ala-Val	C ₄₂ H ₆₆ N ₁₆ O ₈	923.09
DP-035 Trc'n 6;4-10	Trp-His-Arg-Val-Ala-Val-Ile	C ₄₂ H ₆₅ N ₁₃ O ₈	880.07
DP-036 Trc'n 6;5-11	His-Arg-Val-Ala-Val-Ile-Met	C ₃₆ H ₆₄ N ₁₂ O ₈ S	825,05
DP-037 Trc'n 6;6-12	Arg-Val-Ala-Val-Ile-Met-Gly	C ₃₂ H ₆₀ N ₁₀ O ₈ S	744.96
DP-038 Tre'n 4;1-7	Thr-Leu-Phe-Leu-Ala-His-Gly	C ₃₆ H ₅₅ N ₉ O ₉	757.89
DP-039 Trc'n 4;2-8	Leu-Phe-Leu-Ala-His-Gly-Arg	C ₃₈ H ₆₀ N ₁₂ O ₈	812.97
DP-040 Trc'n 4;3-9	Phe-Leu-Ala-His-Gly-Arg-Leu	C ₃₈ H ₆₀ N ₁₂ O ₈	812.98

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PTI-		Structure	Formula	MW
DP-041	1	Leu-Ala-His-Gly-Arg-Leu-Val		
Trc'n				
4;4-10			$C_{34}H_{60}N_{12}O_8$	764.93
		\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		
		NOT MAN		
DP-042	•	Ala-His-Gly-Arg-Leu-Val-Phe		
Trc'n			1	
4;5-11			C ₃₇ H ₅₈ N ₁₂ O ₈	798.95
DP-043		His-Gly-Arg-Leu-Val-Phe-Met		
Trc'n				
4;6-12		Hart Mark Mark Mark Mark Mark Mark Mark Mark	$C_{39}H_{62}N_{12}O_8S$	859.07
		0 1 4 7 0 -		
DP-044		Gly-Leu-Ala-Phe-Val-Leu-Arg		· · · · · · · · · · · · · · · · · · ·
Trc'n		f h i i i h h		
15;1-7		inc.	C ₃₇ H ₆₂ N ₁₀ O ₈	774.97
,-				·
DD 045	•	Los Ala Dha Val Los Ara Clu		
DP-045 Trc'n	·	Leu-Ala-Phe-Val-Leu-Arg-Gly		
15;2-8			C ₃₇ H ₆₂ N ₁₀ O ₈	774.97
,-				
•	•	-M4,		
DP-046		Ala-Phe-Val-Leu-Arg-Gly-Lys		
Trc'n		HAM AND	C ₃₇ H ₆₃ N ₁₁ O ₈	789.98
15;3-9			C371163111108	
		\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		
DP-047		Phe-Val-Leu-Arg-Gly-Lys-Ser	-	
Trc'n				
15;4-10		HAM YOU NOW YOU WILL YOU	C ₃₇ H ₆₃ N ₁₁ O ₉	805.98
ĺ				
	1	HD ATTLE		
DP-048	,	Val-Leu-Arg-Gly-Lys-Ser-Leu		,
Trc'n		ma i l l ~ i l l		
15;5-11		NH NH NH NH NH	$C_{34}H_{65}N_{11}O_{9}$	771.96
		HO HO		
		, ND		
DP-049	<u>.</u>	Leu-Arg-Gly-Lys-Ser-Leu-Tyr	1	•
Trc'n	!			
15;6-2		HAN SHE SHE SHE SHE SHE	$C_{38}H_{65}N_{11}O_{10}$	836.01
		109 NH ₂ NH ₃		
	L .	Fig. 12f	_l	<u> </u>

Fig. 12f

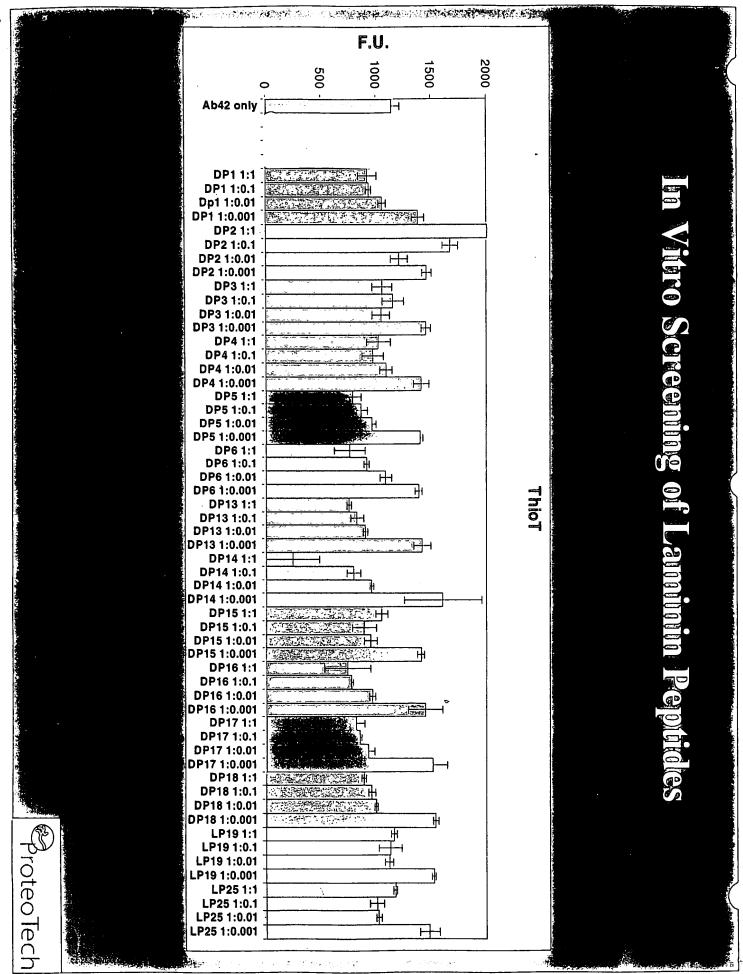
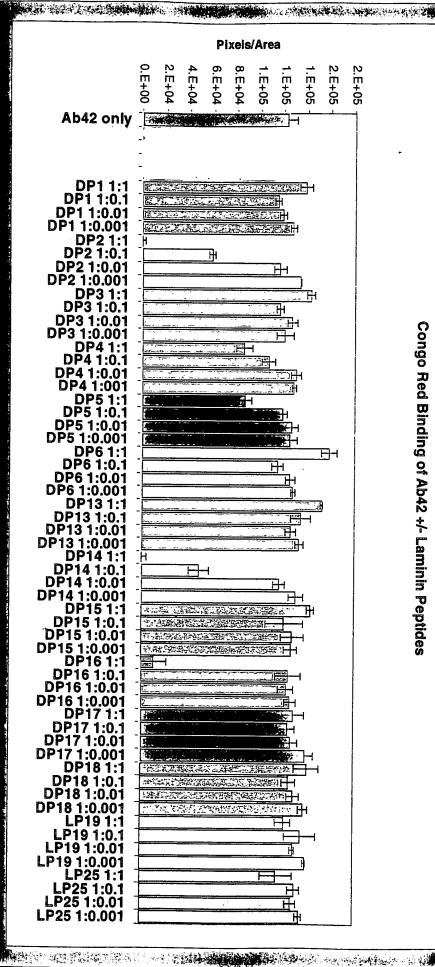


Fig. 13

Vitro Screening of

Congo Red Binding 으 Ab42 +/- Laminin Peptides



Proteo Tech

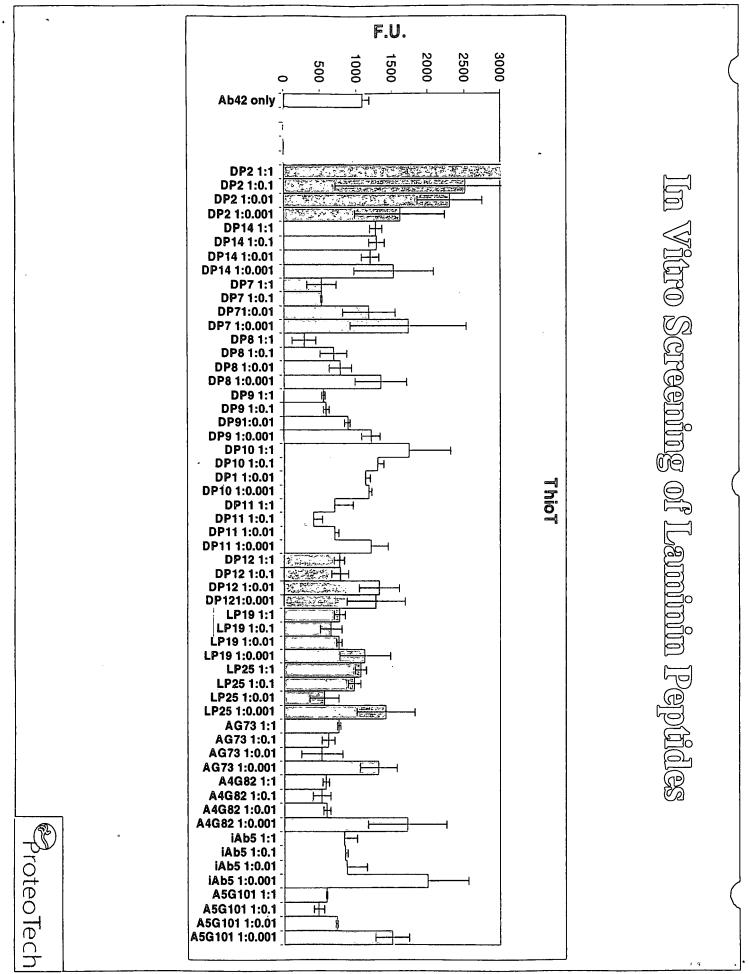


Fig. 15

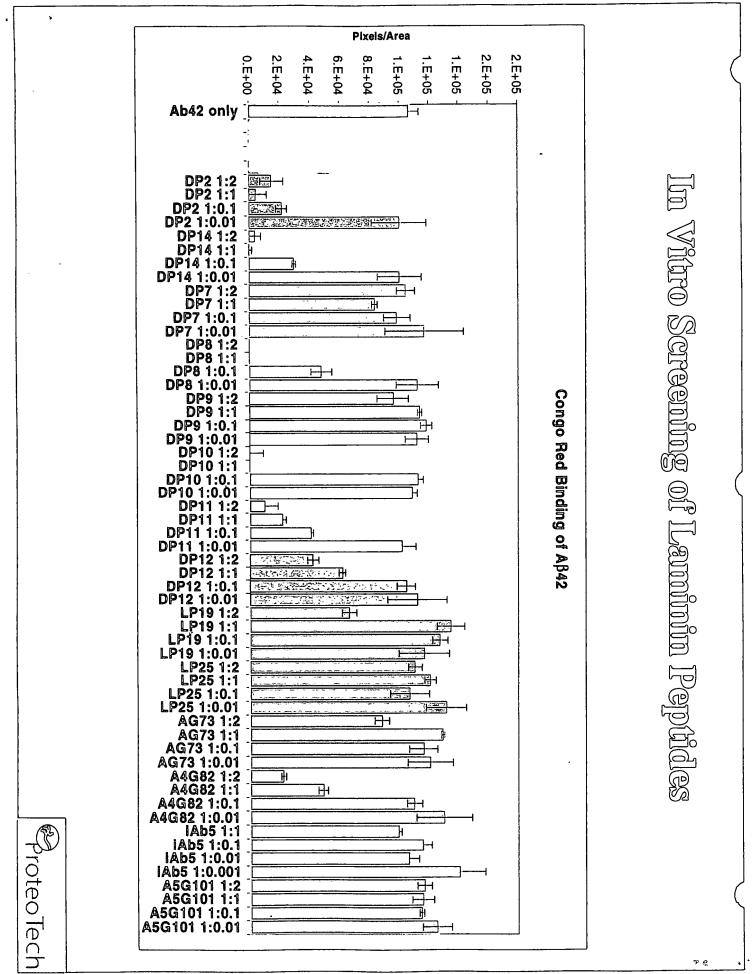


Fig. 16

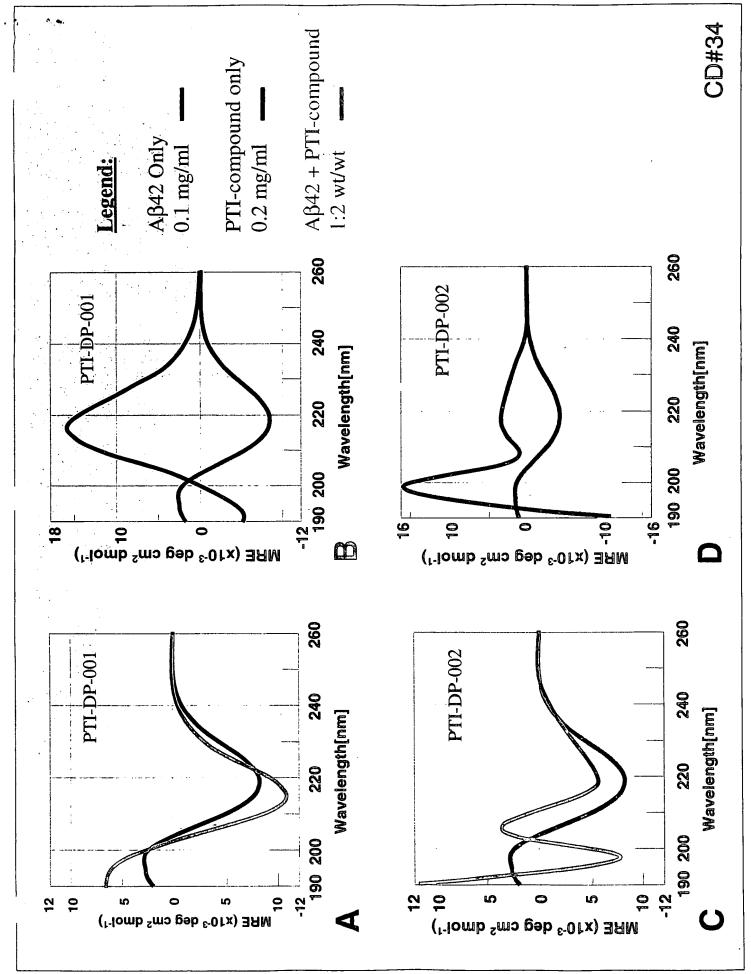


Fig. 17

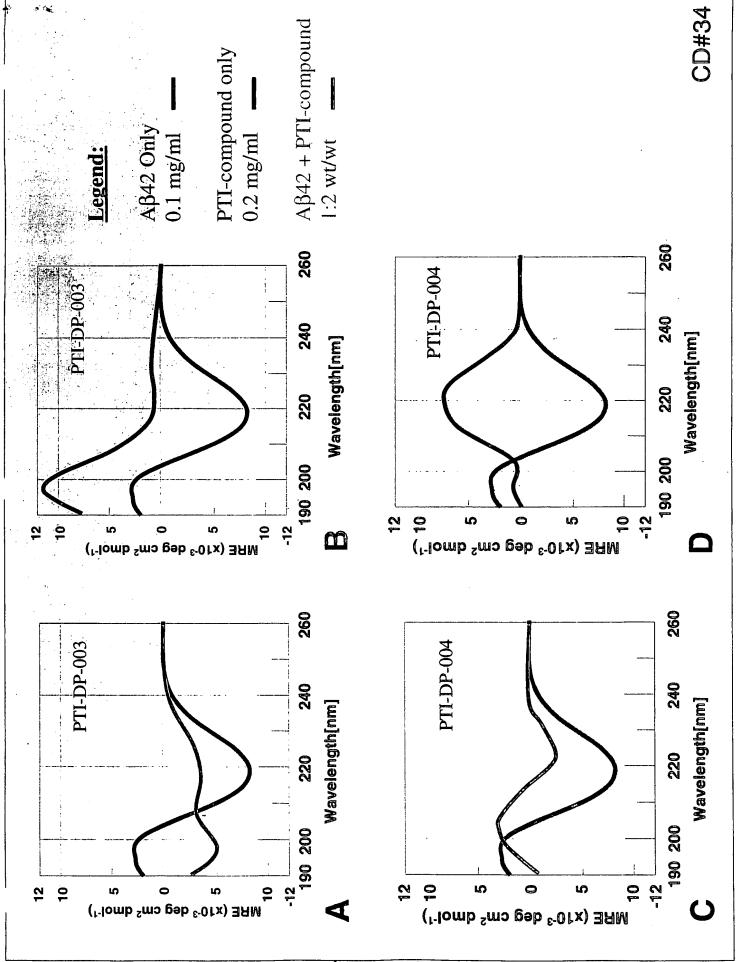


Fig 18

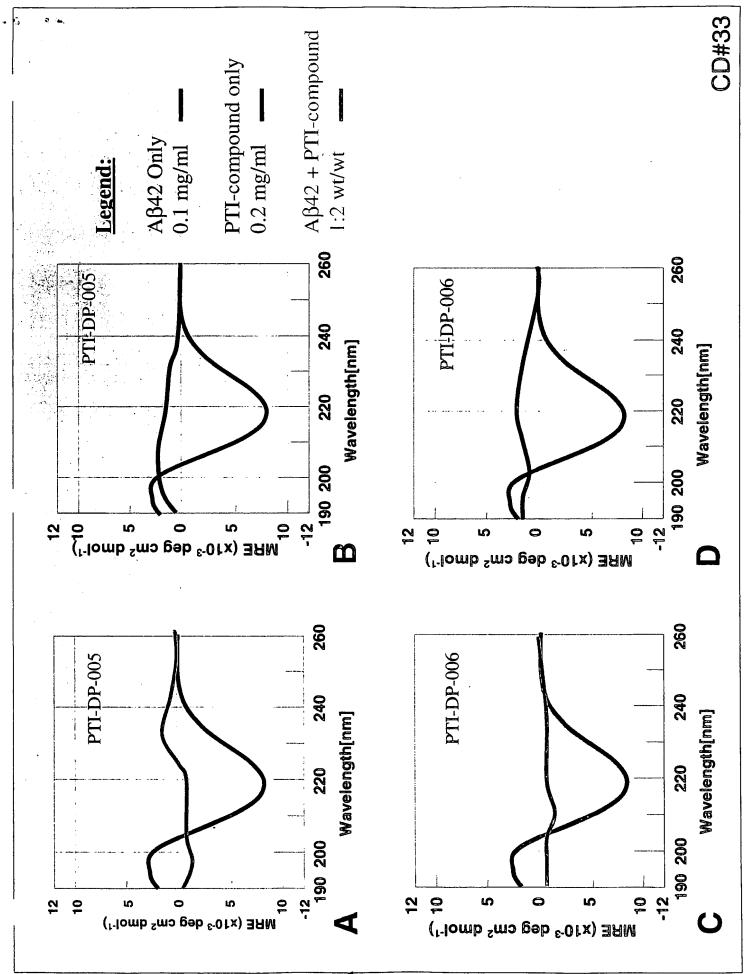


Fig. 19

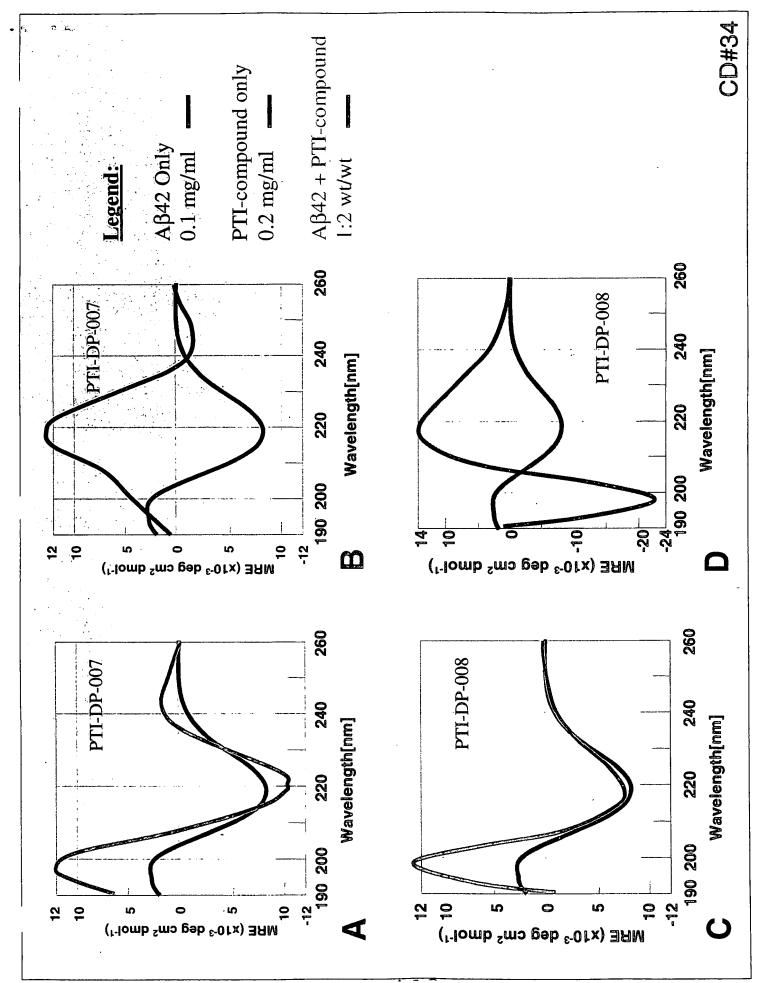


Fig 20

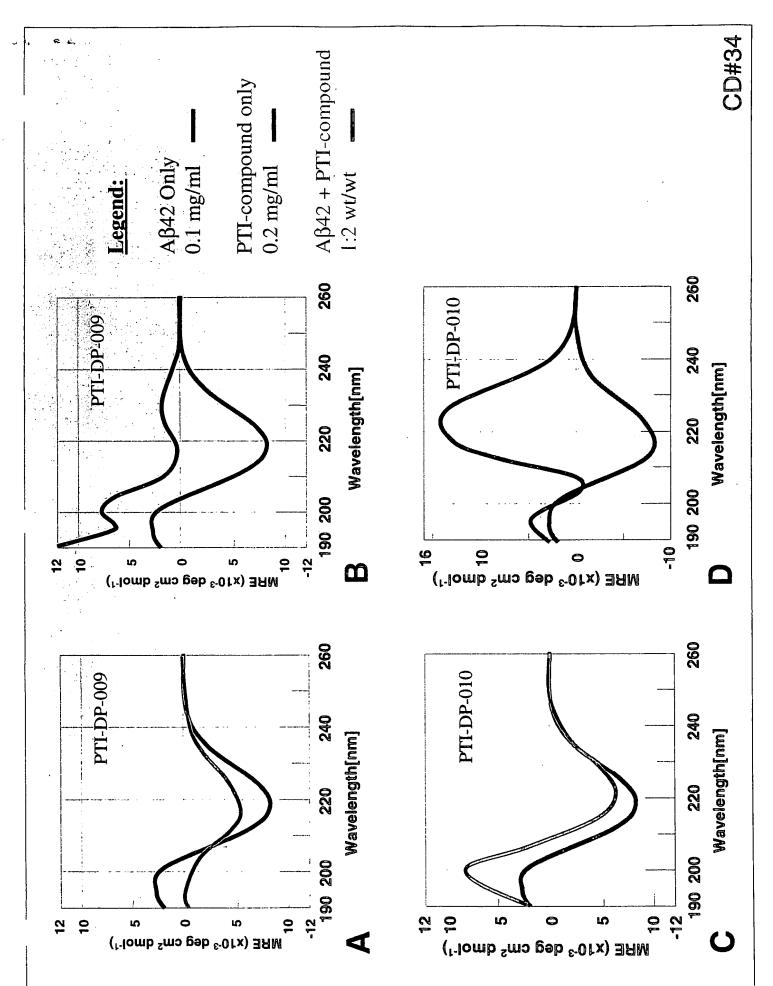


Fig 21

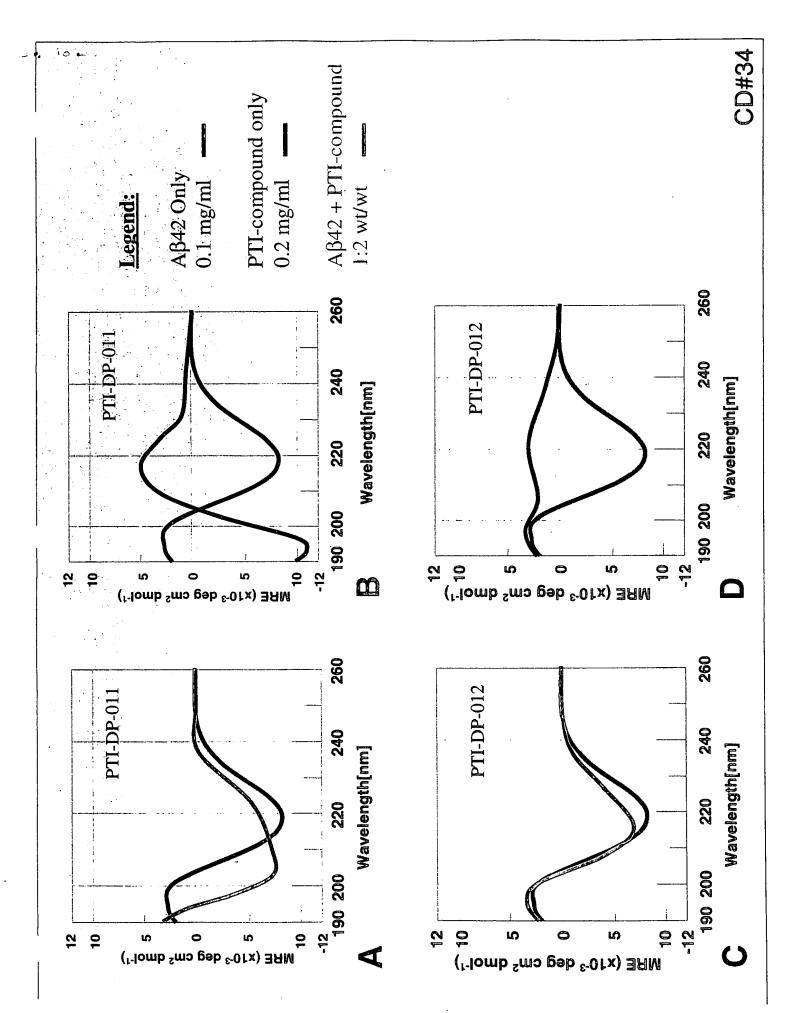


Fig. 22

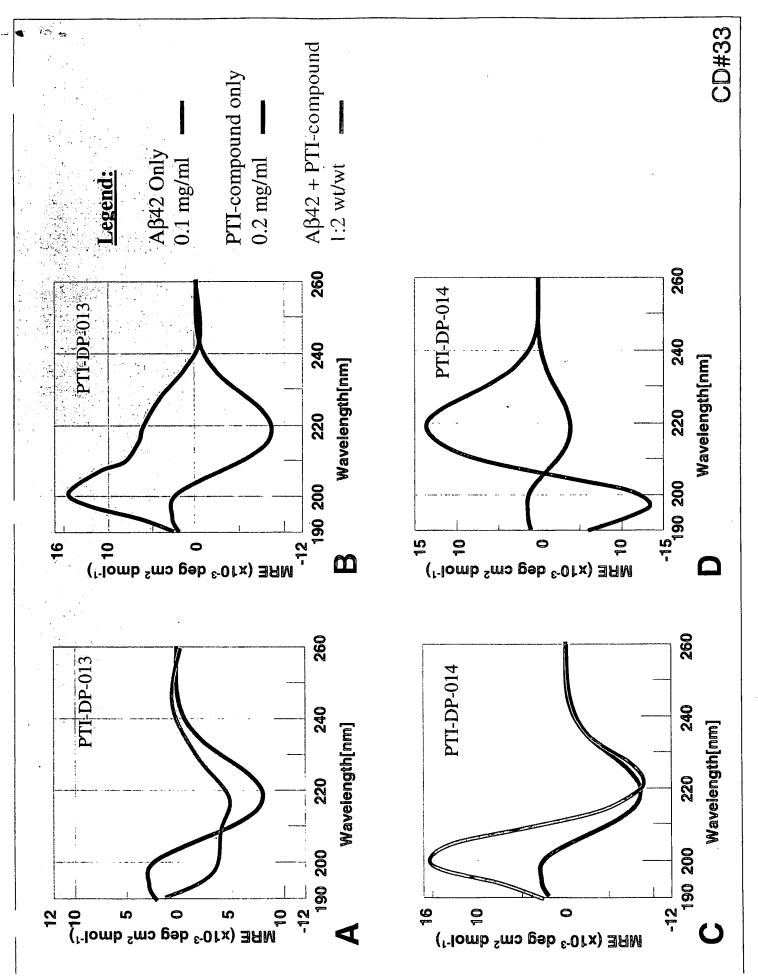


Fig. 23

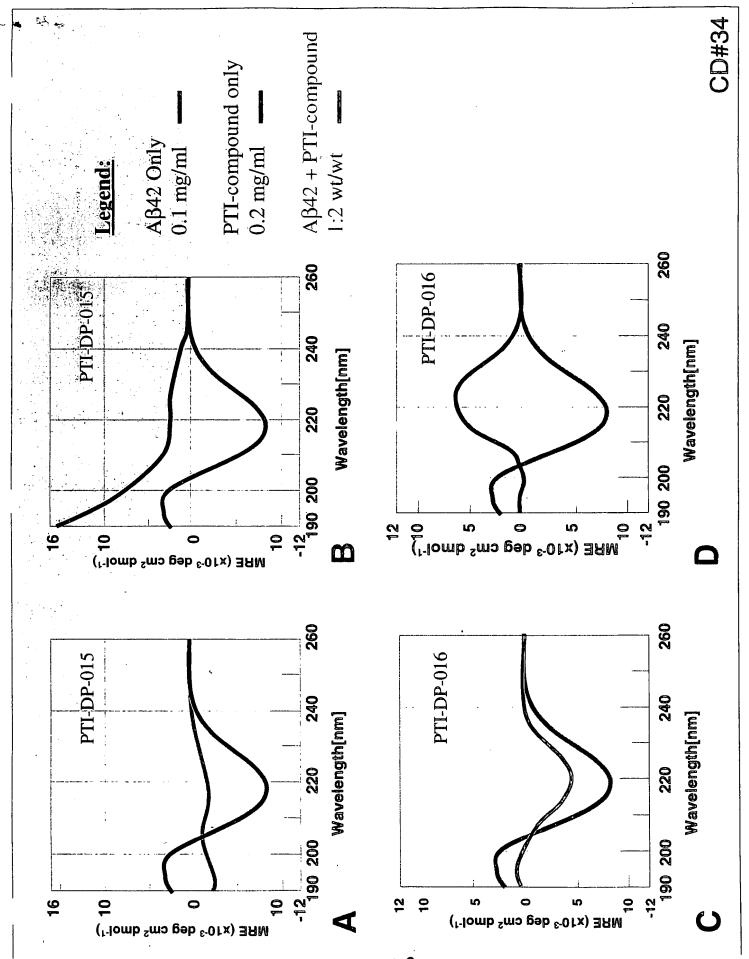


Fig. 24

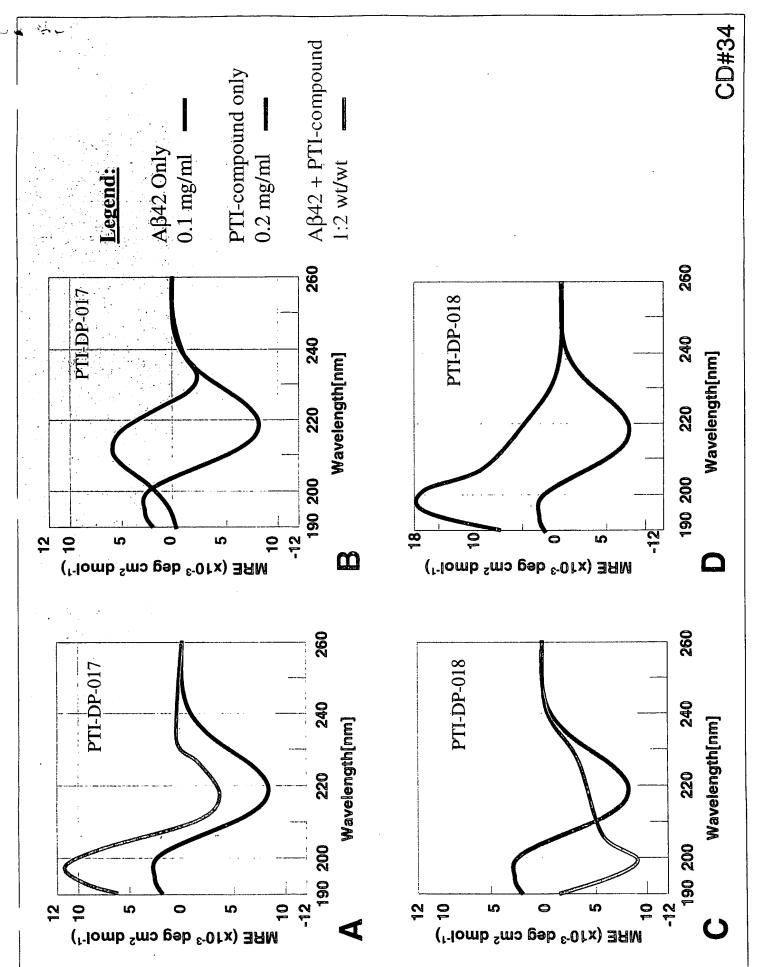


Fig. 25

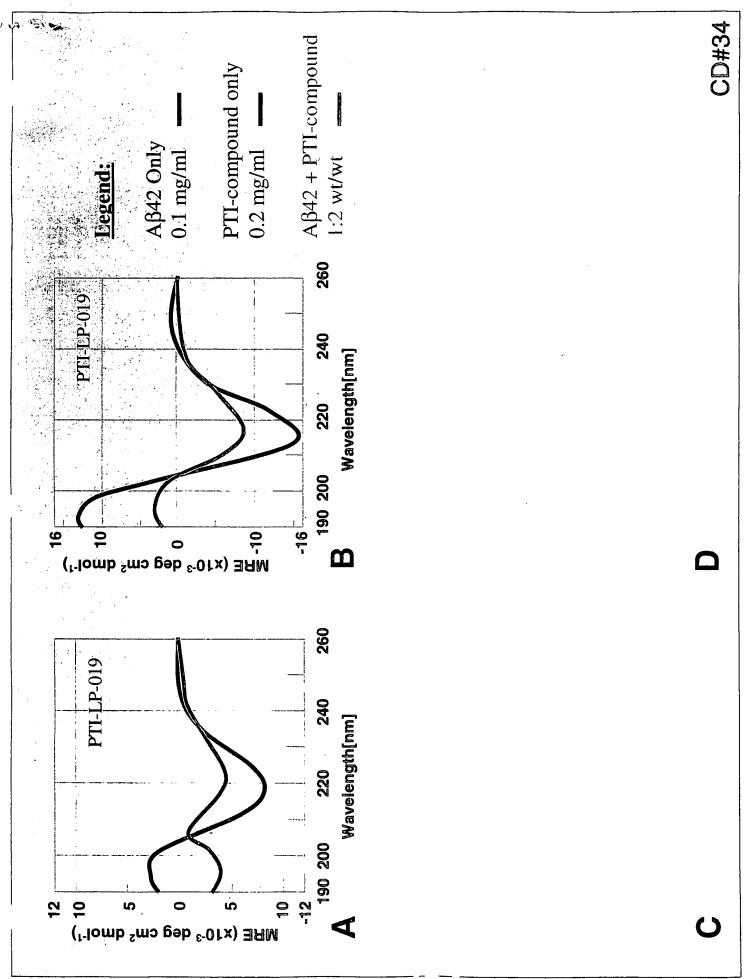


Fig. 26